Supplementary Table 1. Top significant categories identified by Ingenuity Pathway Analysis for pHAR-associated schizophrenia genes.

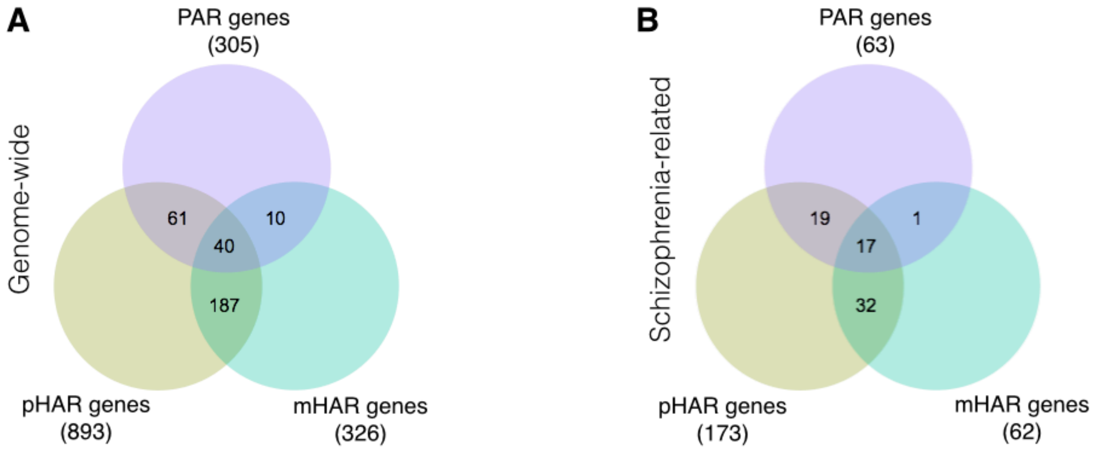
	P-value
Top Canonical Pathways	
Protein Kinase A Signaling	5.41E-05
Ephrin Receptor Signaling	4.64E-04
B Cell Receptor Signaling	2.74E-03
Sertoli Cell-Sertoli Cell Junction Signaling	2.98E-03
Epithelial Adherens Junction Signaling	6.02E-03
Top Molecular and Cellular Functions	
Cellular Development	6.94E-06 - 2.55E-02
Cell Morphology	2.96E-05 - 3.11E-02
Cellular Assembly and Organization	2.96E-05 - 3.11E-02
Cellular Function and Maintenance	2.96E-05 - 2.46E-02
Cell-To-Cell Signaling and Interaction	1.64E-04 - 3.11E-02
Top Physiological System Development and Function	
Nervous System Development and Function	6.94E-06 - 3.11E-02
Tissue Development	6.94E-06 - 3.11E-02
Embryonic Development	2.40E-04 - 2.78E-02
Organ Morphology	3.28E-04 - 3.11E-02
Organismal Development	3.28E-04 - 3.11E-02

Supplementary Table 2. P-values and corrected P-values (in parenthesis) from the INRICH analysis of schizophrenia GWAS regions in genes showing human-specific expression shifts in different organs.

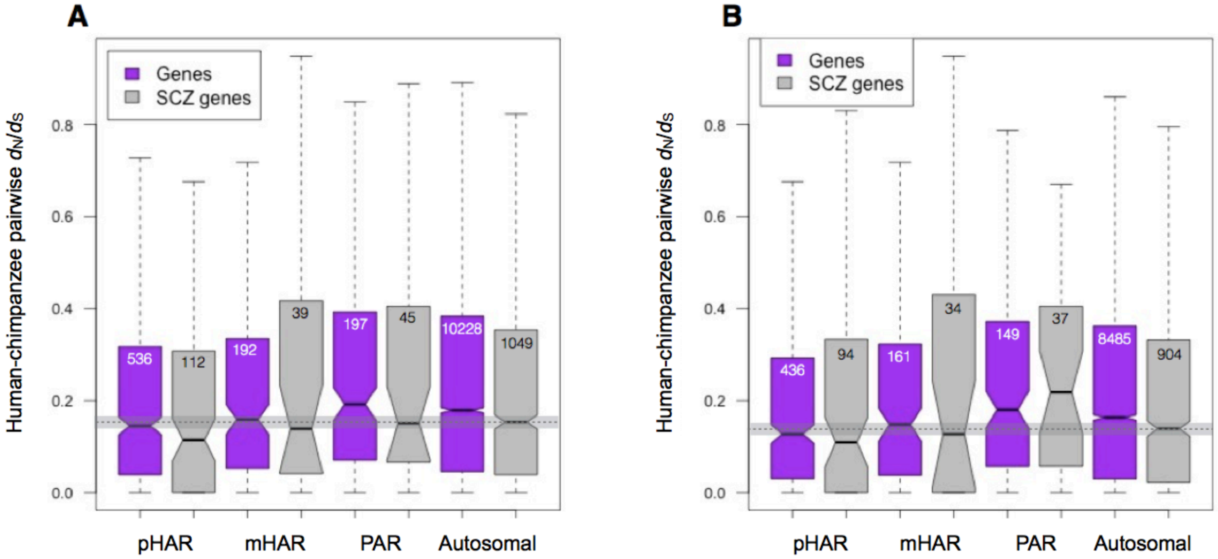
	Cerebellum and Brain	Kidney	Liver	Testis
Nominal P<1e-2	**0.010** (**0.034**)	0.193 (0.518)	0.765 (0.994)	0.495 (0.886)
Nominal P<1e-3	**0.034** (0.116)	0.254 (0.607)	0.691 (0.979)	0.661 (0.966)
Nominal P<1e-4	0.112 (0.326)	0.789 (0.993)	0.759 (0.989)	0.214 (0.583)
Nominal P<1e-5	**0.028** (0.083)	0.550 (0.926)	0.739 (0.985)	0.341 (0.688)
Nominal P<1e-6	**0.026** (0.075)	0.819 (0.994)	1.000 (1.000)	0.087 (0.247)
Nominal P<1e-7	**0.032** (0.092)	0.630 (0.941)	1.000 (1.000)	0.177 (0.464)

Supplementary Table 3. P-values and corrected P-values (in parenthesis) from the INRICH analysis of schizophrenia GWAS regions in genes showing human-specific expression shifts in cerebellum and brain using brain-expressed genes as background.

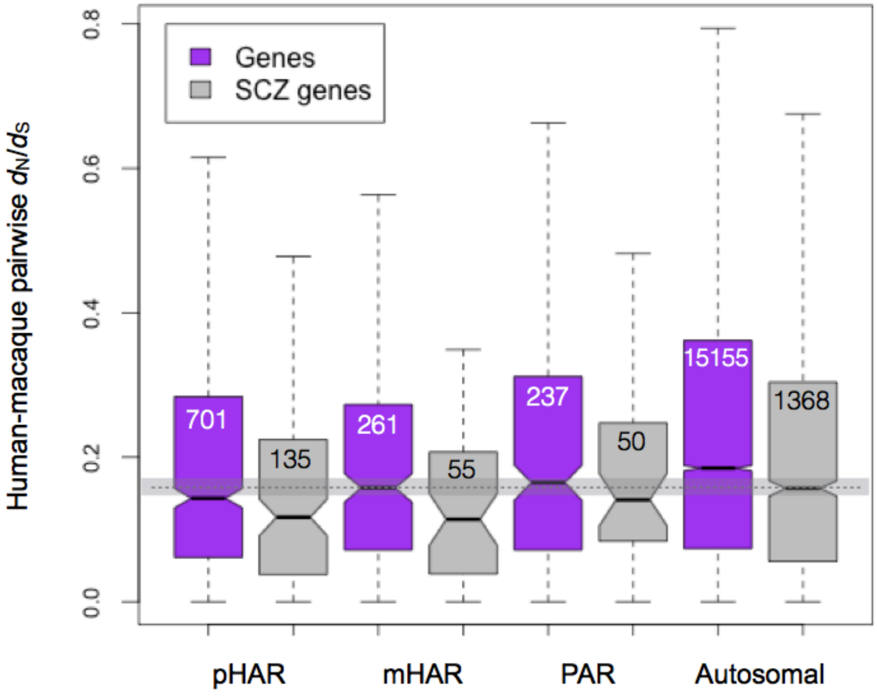
	Cerebellum and Brain	
	Background: genes expressed in the brain	Background: genes highly expressed in the brain
Nominal P<1e-2	**0.036** (**0.035**)	**0.038** (**0.043**)
Nominal P<1e-3	0.195 (0.197)	0.170 (0.172)
Nominal P<1e-4	0.335 (0.325)	0.485 (0.492)
Nominal P<1e-5	0.167 (0.154)	0.375 (0.368)
Nominal P<1e-6	0.080 (0.081)	0.250 (0.252)
Nominal P<1e-7	**0.042** (**0.041**)	0.148 (0.135)



Supplementary Figure 1. A) Number of genes at 100kb flanking regions of pHARs, PARs, and mHARs. B) Number of schizophrenia-related (nominal $P < 1e-4$) genes at 100kb flanking regions of pHARs, PARs, and mHARs.



Supplementary Figure 2. Human-chimpanzee pairwise $d_{\mathrm{N}}/d_{\mathrm{S}}$ comparisons across different sets of genes for A) genes expressed in the brain and B) genes highly expressed in the brain. The purple boxes represent autosomal genes and the ones that are at 100kb flanking regions of pHARs, mHARs, and PARs. The grey boxes represent the intersection of each corresponding gene set with schizophrenia genes under nominal $P < 1e\text{-}4$. Number of genes after filtering is given in the box for each category. Outliers are omitted from the plots. For both plots, the horizontal shade represents median $d_{\mathrm{N}}/d_{\mathrm{S}}$ and its confidence interval of all the schizophrenia genes (the last box).



Supplementary Figure 3. Human-macaque pairwise d_N/d_S comparison across different sets of genes. The purple boxes represent autosomal genes and the ones that are at 100kb flanking regions of pHARs, mHARs, and PARs. The grey boxes represent the intersection of each corresponding gene set with the schizophrenia genes under nominal $P < 1e-4$. Number of genes after filtering is given in the box for each category. Outliers are omitted from the plot. The horizontal shade represents median d_N/d_S and its confidence interval of all the schizophrenia genes (the last box).